



## Variability and Traits Association Analyses in Maize (*Zea mays* L.) Genotypes

Masuma Rahman, Ahasanul Hoque, Md. Amir Hossain, Md. Abdullah Al Bari\*

*Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh-2202, Bangladesh*

\*Corresponding author and Email: [abdullahgpb@gmail.com](mailto:abdullahgpb@gmail.com)

Received: 25 January 2017

Accepted: 22 December 2017

### Abstract

An experiment was conducted at the experimental farm of the Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh with fifteen maize (*Zea mays* L.) genotypes to assess the genetic variability, characters association and divergence among the genotypes for yield and yield attributing traits. The experiment was conducted during November 2015 to May 2016, following Randomized Complete Block Design (RCBD) with three replicates in two adjacent environments to discern the performance of the genotypes in interacting environments. No significant variation was observed for environments, which was perhaps due to their close proximity. The genotypes differed significantly for most of the studied traits. The phenotypic co-efficient of variation (PCV) was higher than genotypic co-efficient of variation (GCV) for all the evaluated traits. High heritability along with high genetic advance was observed for 1000 seed weight, seed numbers ear<sup>-1</sup> and yield plant<sup>-1</sup>. Yield plant<sup>-1</sup> was significantly associated with plant height, ear length, ear girth, husk girth, kernel length, 1000 seed weight, kernel numbers row<sup>-1</sup>, seed numbers ear<sup>-1</sup> in positive direction and negatively associated with days to anthesis and moisture loss (%). Path co-efficient analysis revealed that the maximum positive direct contribution towards yield was through 1000 seed weight, seed number ear<sup>-1</sup> and kernel length whereas plant height, ear girth, ear length, kernel numbers row<sup>-1</sup> showed negative direct contribution towards yield due to negative indirect effects of several parameters. Cluster analysis exhibited five distinct groups. Considering mean values Cluster II provided the best result in terms of yield and earliness, followed by Cluster IV and V. The results of principal component analysis (PCA) revealed that first five components accounted for 82.7% of total variation. The findings indicate the presence of ample genetic diversity among maize genotypes which can be exploited in future breeding program for better utilization of maize germplasm.

**Keywords:** Maize, Variability, Heritability, Characters association, PCA, Cluster analysis.

### 1. Introduction

Maize (*Zea mays* L.), one of the overriding grain crops, plays a significant role in human and livestock nutrition globally, thus contributes in alleviating the acute shortage of food. To date, maize is widely cultivated around the world, over a wide range of environmental conditions

signifying its global and regional importance to millions of people relying on the crop in the pursuit of food security and livelihoods. The fast-growing maize crop is very promising in Bangladesh for its multipurpose uses, with added values. The poultry, dairy, fisheries industries are increasing very rapidly in Bangladesh demanding more quality feed, thus, increasing

maize production is gaining prime necessity. In the year 2014-15, maize cultivation occupied 804 thousand acres with the production of 227200 metric tons in Bangladesh and countries average yield of maize was 2826kg per acre on the same year (BBS, 2016). The acreage and production of maize in the country is increasing but not encouraging enough compared to the world perspective, and the demand of the crop in the country is increasing at a higher rate. To meet the ever increasing demand of increasing population of Bangladesh maize breeders need to pay special attention to investigate the genetic diversity of maize that could develop genotypes with higher yield and better quality. The availability of adequate genetic diversity is crucial for gaining significant genetic progress in applied breeding programs. Yield of maize like rest crops is the final product attributed by a complex chain of interrelating effects of different characters (Singh *et al.*, 2005). Therefore, the knowledge of association among characters with yield is precious to plant breeders as it helps in the selection of traits as well as genotypes with better accuracy. The correlation coefficient indicates the degree of association between characters for the selection of desirable characters in a breeding program. For any crop improvement programs genetic variation and its analysis are important components (Mohammadi *et al.*, 2003) in planning and executing breeding programs. High germplasm diversity for yield and yield attributing characters has an important role in developing prime varieties.

As all crop breeding programs aim to amplify yield capacity which is the universal objective, here the concern is to characterize the quality attributes of 15 maize genotypes to assess the genetic diversity among them for isolating potential genotypes that can be utilized for future plant breeding programs as a prerequisite of achieving potential hybrids or improving maize genotypes. Accordingly, the present study was carried out with the objective of generating information on variabilities, and relationship among yield and yield contributing traits to find important traits for selection process.

## 2. Materials and Methods

### 1.1. The genotypes, study area and experimental design

The experiment material for the present investigation comprised of five commercial hybrids (BHM-3, BHM-5, BHM-6, BHM-7, BHM-9), five half sib indigenous populations (Indigenous Purple, Indigenous Yellow-1, Indigenous Yellow-2, E155-1, E155-2) and five hybrid derived F<sub>2</sub> generation (BHM-3 derived F<sub>2</sub>, BHM-5 derived F<sub>2</sub>, BHM-6 derived F<sub>2</sub>, BHM-7 derived F<sub>2</sub>, BHM-9 derived F<sub>2</sub>) were studied in two adjacent locations as environments following Randomized Complete Block Design with three replications at the experimental farm of the Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh during the period from November, 2015 to May, 2016. Each plot consisted of single row of 3.5 m long where row to row distance was 0.6 m and block to block distance was 1 m.

### 1.2. Data collection

Observation was recorded on five randomly selected plants of each plot for fifteen important characters. These characters were days to anthesis, plant height (cm), ear height (cm), stalk lodging (%), moisture loss (%), ear length (cm), ear girth (cm), husk girth (cm), kernel length (cm), number of rows ear<sup>-1</sup>, kernels row<sup>-1</sup>, number of seeds ear<sup>-1</sup>, 1000 seed weight (g), grain yield plant<sup>-1</sup> (g). Analysis of variance was performed using the statistical software Statistical Analysis System (SAS, version 9.3), genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.* (1995). Heritability in broad sense ( $h^2_b$ ) was estimated according to the formula suggested by Johnson *et al.* (1955) and Hanson (1961). Genotypic and phenotypic co-efficient of variations were estimated according to Burton (1952) and Singh and Choudhury (1985). Genetic advance was calculated following formula given by Johnson *et al.* (1955) and Allard (1975). Genetic advance in percent of mean was calculated by the formula of Comstock *et al.*, (1952). The phenotypic

correlations were estimated by the formula suggested by Miller *et al.* (1958). Correlation coefficient were further partitioned into components of direct and indirect effects by path coefficient analysis originally developed by Wright (1921) and later described by Dewey and Lu (1959). Cluster analysis and principal component analysis (PCA) were done using R software (R Core Team, 2016).

### 3. Results and Discussion

In combined analysis of variance, significant variation were observed among the genotypes for all the traits studied except stalk lodging (%) and row numbers ear<sup>-1</sup> (Table 1). Significant variation among genotypes indicated the presence of genotypic differences suggesting the importance of their genetic value in order to identify the best genetic makeup for a particular condition, thereby provide better scope of selection. Ghimire *et al.*, (2015) observed significant variations among the genotypes for the traits grain yield, ear weight, number of kernel row<sup>-1</sup>, number of kernel ear<sup>-1</sup>, ear length, ear girth, plant height, ear height that supports findings of the research. In terms of earliness BHM-7 was the best as the genotype required the minimum number of days to anthesis (92.5 days), followed by E155-2 (93.67 days), BHM-6 (94.17 days), BHM-9 derived F<sub>2</sub> (94.83 days), BHM-7 derived F<sub>2</sub> (94.83 days). Plant height ranged from 142 cm (indigenous yellow-2) to 185.58 cm (BHM-9).

The highest ear height (96.08cm) was observed in indigenous yellow-2, whereas the lowest value (61.17) was recorded in BHM-5 derived F<sub>2</sub>. The highest ear length (21.32) was observed in BHM-9. BHM-7 had the highest ear girth, maximum kernel length and seed numbers ear<sup>-1</sup>. The genotype E155-1 gave the highest number of kernel row<sup>-1</sup>. The genotype BHM-6 gave the highest mean value for 1000 seed weight (384.17g). The highest yield per plant (172.85g) was observed in BHM-7, followed by BHM-9, BHM-6, BHM-9 derived F<sub>2</sub>, BHM-3, E155-1,

E155-2, where Indigenous purple produced minimum yield (39.17g) (Table 2).

#### 3.1. Genetic parameter analysis

A clear idea can be gained on the actual strength of variability by comparing the relative amount of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). The PCV was higher than GCV for all the studied traits (Table 3) indicates that environmental conditions influence their phenotypic expression. Ababulgu (2014) reported the same. Days to anthesis, plant height, ear length, ear girth, 1000 seed weight showed relatively low difference between PCV and GCV. This indicates the low impact of environment on the expression of characters and hence, they could be improved by following different phenotypic selections like directional, disruptive and stabilized selections.

Heritability was classified as low (below 30%), medium (30-60%) and high (above 60%) as suggested by Johnson *et al.*, (1955). The highest heritability (84.75%) was observed in 1000 seed weight, followed by yield plant<sup>-1</sup>, ear length, ear girth, plant height and days to anthesis. Highest genetic advance was noticed for 1000 seed weight (204.27). Highest genetic advance as percent of mean was observed for yield plant<sup>-1</sup> followed by 1000 seed weight (Table 3). In the present experiment high heritability with high genetic advance was observed for the traits 1000 seed weight, yield plant<sup>-1</sup>, seed numbers ear<sup>-1</sup> and plant height. High genetic advance coupled with high heritability was observed by Kinfe and Tsehaye (2015) for plant height and grain yield. Bekele and Rao (2014) recorded high genetic advance with higher heritability for 100 seed weight which is similar with the present finding. Rahman *et al.* (2015) also found the same result for 1000-kernel weight. These traits can be improved through simple or progeny selection methods. Other traits that showed high to low heritability along with moderate to low genetic advance can be improved by inter-mating superior genotypes of segregating populations.

**Table 1.** Analysis of variance (mean square) for different characters of 15 maize genotypes

Source of Variance	DF	DA	PH	EH	SL	ML	EL	EG
Environment	1	36.1	1587.6	783.22	191.55	77.93	23.54	10.08
Replication (Env.)	4	35.73	521.36	202.71	493.02	34.96	5.72	2.49*
Genotypes	14	162.9***	1467.89***	565.80**	266.98	189.98**	58.92***	11.44***
Env.*Geno.	14	23.48	221.64	107.81	180.18	46.77	2.81	1.1
Error	56	24.64	187.09	109.62	257.74	37.76	4.16	0.87

..... Continued Table 1

Source of Variance	HG	KL	RN	KR	SN	Wt	YP
Environment	6.18	0.47	10.68	86.04	22294	12532	8.36
Replication (Env.)	1.05	0.76	1.12	40.04	8059.76	3076.66	615.58
Genotypes	1.73*	5.55***	5.14	113.58**	25350**	36894***	10858***
Env.*Geno.	0.56	0.8	2.08	26.37	4590.35	1014.81	772.64
Error	0.54	0.75	1.4	20.42	4689.5	2087.67	711.72

\*, \*\*, \*\*\* indicates significance at  $P < 0.05$ ,  $< 0.01$  and  $< 0.001$  respectively

Here, DA= Days to anthesis, PH= Plant height (cm), EH= Ear height (cm), SL=Stalk lodging (%), ML= Moisture loss (%), EL= Ear length (cm), EG= Ear girth (cm), HG= Husk girth (cm), KL= Kernel length (cm), RN= Row numbers ear<sup>-1</sup>, KR= Kernel numbers row<sup>-1</sup>, SN= Seed numbers ear<sup>-1</sup>, Wt= 1000 seed weight (g), YP=Yield plant<sup>-1</sup> (g), Env.=Environment, Geno.=Genotypes, Replication(Evn.)= Replication within environment.

**Table 2.** Average performance for different traits of 15 maize genotypes

Genotype	DA	PH	EH	SL	ML	EL	EG	HG	KL	RN	KR	SN	Wt	YP
Indigenous Purple	109.83	150.25	95.08	17.36	22.42	12.2	10.93	8.18	2.74	16	21.08	283.67	139.17	39.17
Indigenous Yellow 1	108.67	142.33	91.83	17.77	28.66	12.17	13.18	9.23	3.95	16.67	20.42	306.42	172.5	56.26
Indigenous Yellow 2	104	142	96.08	18.75	22.6	11.19	12.82	9.62	3.2	15	20.92	281.08	143.33	43.63
E155-2	93.67	166.67	75.83	20.38	11.06	17.29	13.79	9.18	4.61	13.5	30.17	408.5	320	130.88
E155-1	99	163.42	70.83	5.17	11	19.11	14.23	9.17	5.06	14.33	33.67	458.17	305.83	140.09
BHM-9	96.67	185.58	84	24.51	11.36	21.32	15.15	9.46	5.69	14.33	33.33	456.75	357.5	163.08
BHM-5	96.33	179.08	86.25	20.17	12.48	19.16	13.45	8.88	4.57	13.83	27.17	371.58	319.17	118.51
BHM-6	94.17	167.5	80.67	15.64	19.65	19.68	15.73	10.08	5.64	13.83	29.92	401.5	384.17	153.30
BHM-3	98.33	181.58	86.5	9.96	14.17	19.9	14.28	9.02	5.26	13.83	30.83	442.17	316.67	142.92
BHM-7	92.5	183.17	83.17	12.1	10.32	19.46	16.58	10.21	6.37	15	29.75	466.67	370.83	172.85
BHM-9 F <sub>2</sub>	94.83	166	73.75	24.89	10.12	19.35	13.99	9.17	4.83	14.83	30.92	434.75	340	147.06
BHM-5 F <sub>2</sub>	97.67	143.08	61.17	12.66	12.45	16.98	12.78	8.46	4.32	14	24.5	308.83	292.5	88.79
BHM-6 F <sub>2</sub>	96.67	171.42	80.58	14.34	13.57	18.52	15.25	9.7	5.55	14.5	25.5	358.83	340.83	121.19
BHM-3 F <sub>2</sub>	99.33	147.83	74.58	12.78	16.62	16.95	13.14	9	4.15	13.17	25.67	342.17	282	94.81
BHM-7 F <sub>2</sub>	94.83	151.42	71.58	16.45	11.23	15.91	14	9.34	4.65	14.67	26.33	383	275.83	105.74
Min.	92.50	142.00	61.17	5.17	10.12	11.19	10.93	8.18	2.74	13.17	20.42	281.08	139.17	39.17
Max.	109.83	185.58	96.08	24.89	28.66	21.32	16.58	10.21	6.37	16.67	33.67	466.67	384.17	172.85
Avr.	98.43	162.76	80.79	16.19	15.18	17.28	13.95	9.24	4.71	14.50	27.34	380.27	290.69	114.55
SE	1.28	3.53	2.70	4.15	1.59	0.53	0.24	0.19	0.22	0.31	1.17	17.68	11.80	6.89
LSD (5%)	7.94	21.89	16.76	25.69	9.83	3.26	1.49	1.18	1.39	1.89	7.23	109.59	73.12	42.69
CV%	5.04	8.40	12.96	99.13	40.48	11.80	6.69	7.95	18.40	8.16	16.53	18.01	15.72	23.29

Here DA= Days to anthesis (days), PH= Plant height (cm), EH= Ear height (cm), SL=Stalk lodging (%), ML= Moisture loss(%), EL= Ear length (cm), EG= Ear girth (cm), HG= Husk girth (cm), KL= Kernel Length (cm), RN= Row numbers ear<sup>-1</sup>, KR= Kernel numbers row<sup>-1</sup>, SN= Seed numbers ear<sup>-1</sup>, Wt= 1000 seed weight (g), YP= Yield per plant (g), Min.= Minimum, Max. = Maximum, Avr.= Average, SE= Standard Error, SD= Standard Deviation, LSD (5%)= Least Significant Difference at 5% level of Probability, CV%= Coefficient of Variation.

**Table 3.** Genetic Parameter of different characters of 15 maize genotypes

Traits	GV	PV	Heritability (%)	GCV %	PCV %	GA	GA (%)
DA (days)	46.09	70.73	65.16	6.89	8.54	11.29	11.47
PH (cm)	426.93	614.02	69.53	12.69	15.22	35.49	21.81
EH (cm)	152.06	261.68	58.11	15.262	20.02	19.36	23.97
SL (%)	28.93	209.11	13.84	33.21	89.29	4.12	25.44
ML (%)	50.74	88.5	57.33	46.92	61.97	11.11	73.19
EL (cm)	18.25	22.41	81.44	24.72	27.39	7.94	45.96
EG (cm)	3.52	4.39	80.2	13.45	15.02	3.46	24.82
HG (cm)	0.39	0.94	42.35	6.76	10.49	0.84	9.13
KL (cm)	1.6	2.35	68.09	26.87	32.57	2.15	45.68
RN	1.25	2.65	47.1	7.71	11.23	1.58	10.89
KR	31.05	51.47	60.33	20.38	26.24	8.92	32.61
SN	6886.83	11576.3	59.49	21.82	28.29	131.86	34.67
Wt (g)	11602.1	13689.8	84.75	37.05	40.25	204.27	70.27
YP (g)	3382.09	4093.81	82.61	50.77	55.86	108.89	95.05

Here, DA= Days to anthesis (days), PH= Plant height (cm), EH= Ear height (cm), SL=Stalk lodging (%), ML= Moisture loss(%), EL= Ear length (cm), EG= Ear girth (cm), HG= Husk girth (cm), KL= Kernel Length (cm), RN= Row numbers ear<sup>-1</sup>, KR= Kernel numbers row<sup>-1</sup>, SN= Seed numbers ear<sup>-1</sup>, Wt= 1000 seed weight (g), YP= Yield plant<sup>-1</sup> (g).

### 3.2. Correlation co-efficient studies

A crop breeding program aimed at increasing the yield requires consideration not only of yield but also of its associated components that have direct or indirect impact on yield. Correlation coefficient analyses measures the mutual relationship among various plant characters and determines the point on which selection can be based for improving yield.

Phenotypic correlation co-efficient studies were done in this experiment among all the traits (Table 4) in all possible combinations to know the nature of relationship among them. Yield plant<sup>-1</sup> showed highly significant positive correlation with plant height, ear length, ear girth, husk girth, kernel length, kernel numbers row<sup>-1</sup>, seed numbers ear<sup>-1</sup> and 1000 seed weight. Rahman *et al.* (2016), found positive and significant correlation of kernel yield with ear length, grain weight and this result is similar to the present experimental findings. Grain yield was positively and strongly correlated with ear length and diameter, ear height and plant height according to Kinfe and Tsehaye (2015). Beiragi *et al.*, (2011) reported that ear girth and number of kernels per row had the highest correlation with grain yield. Positive significant correlation between plant height and yield plant<sup>-1</sup> had also been reported by Salami *et al.* (2007) and Rafiq *et al.* (2010).

Yield plant<sup>-1</sup> was negatively but significantly correlated with days to anthesis and moisture loss (%) whereas insignificant association was found with ear height (cm) and row numbers ear<sup>-1</sup>. The negative and non-significant association referred a complex linked of relation among the pair of combinations. The findings suggested that the selection of genotypes having higher ear length, ear girth and kernel length, lower days to anthesis, high seed numbers ear<sup>-1</sup> and high 1000 seed weight should be the priority of breeders to achieve higher yield.

Morphological traits which do not show any significant association or very negligible amount of association can be discarded to reduce the

number of traits to be characterized. This correlation can be used as basis for character discard if similar research is conducted in the future using additional morphological traits. Elimination of excessive traits will not only reduce the workload of researcher but also will make characterization less cumbersome and more efficient.

### 3.3 Path analysis

Yield is the function of many component characters which directly or indirectly contributed to it. Correlation studies give an idea about the positive and negative associations of different characters with yield and also among themselves. But the nature and extent of contribution of these characters towards yield is not obtained. Path coefficient analysis was used to make partition of the correlation coefficient of the different characters studied to know direct and indirect effects on yield. The information obtained helps in giving proper importance to the various characters during selection or other breeding program so that the improvement of desirable traits can be achieved effectively. Path coefficient analysis (Table 5) revealed that days to anthesis, ear height, moisture loss (%), husk girth, kernel length, seed numbers ear<sup>-1</sup> and 1000 seed weight had direct positive effect on yield plant<sup>-1</sup>, indicating these are the parameters that contributed yield the most. Whereas days to anthesis, ear height, moisture loss (%) were negatively correlated with yield plant<sup>-1</sup>. This negative effect of days to anthesis mainly was due to the fact that positive direct effect of days to anthesis on yield was nullified by its negative indirect effects of 1000 seed weight and seed numbers ear<sup>-1</sup>. Similarly negative effect of ear height was due to the fact that positive direct effect of this trait on yield was nullified by its negative indirect effect of 1000 seed weight and seed numbers ear<sup>-1</sup> and the same occurred for moisture loss (%). Munawar (2013) found more or less similar result that cob height, number of grains per row and cob girth had high positive direct effects on grain yield, and negative direct effects were showed by plant height and cob length.

**Table 4.** Phenotypic correlation co-efficient between yield and yield attributing traits

	YP	DA	PH	EH	SL	ML	EL	EG	HG	KL	RN	KR	SN	Wt
YP	1.00	-0.65***	0.61***	-0.17	0.14	-0.51***	0.85***	0.73***	0.36***	0.72***	-0.2	0.76***	0.85***	0.87***
DA		1	-0.33**	0.29**	0.07	0.43***	-0.54***	-0.47***	-0.25*	-0.45***	0.32**	-0.47***	-0.5***	-0.65***
PH			1	0.45***	0.03	-0.42***	0.6***	0.53***	0.26*	0.53***	-0.2	0.41***	0.49***	0.54***
EH				1	0.08	0.17	-0.22*	-0.03	0.12	-0.14	0.16	-0.18	-0.11	-0.26*
SL					1	-0.03	0.11	0.02	0.12	-0.06	0.08	0.2	0.22*	0.03
ML						1	-0.54***	-0.37***	-0.17	-0.38***	0.27*	-0.46***	-0.46***	-0.52***
EL							1	0.65***	0.28**	0.67***	-0.35**	0.73***	0.68***	0.83***
EG								1	0.69***	0.84***	-0.01	0.45**	0.56***	0.69***
HG									1	0.19	0.06	0.2	0.31**	0.31**
KL										1	-0.06	0.46***	0.53***	0.7***
RN											1	-0.22*	-0.02	-0.35**
KR												1	0.86***	0.52***
SN													1	0.51***
Wt														1

\*, \*\*, \*\*\* indicates significance at  $P < 0.05$ ,  $< 0.01$  and  $< 0.001$  respectively

Here, DA= Days to anthesis, PH= Plant height (cm), EH= Ear height (cm), SL=Stalk lodging (%), ML= Moisture loss (%), EL= Ear length (cm), EG= Ear girth (cm), HG= Husk girth (cm), KL= Kernel length (cm), RN= Row numbers ear<sup>-1</sup>, KR= Kernel numbers row<sup>-1</sup>, SN= Seed numbers ear<sup>-1</sup>, Wt= 1000 seed weight (g), YP= Yield plant<sup>-1</sup> (g).



**Table 5.** Partitioning of phenotypic correlation coefficients into direct and indirect effects of 13 important traits of 15 maize genotypes by path analysis

	DA	PH	EH	SL	ML	EL	EG	HG	KL	RN	KR	SN	Wt	Correlation with YP
DA	<b>0.003</b>	0.002	0.014	0.000	0.029	0.018	0.129	-0.036	-0.102	-0.003	0.022	- 0.307	-0.418	<b>-0.65***</b>
PH	-0.001	<b>-0.005</b>	0.021	0.000	-0.029	-0.019	-0.146	0.037	0.120	0.002	-0.019	0.301	0.347	<b>0.61***</b>
EH	0.001	-0.002	<b>0.047</b>	0.000	0.012	0.007	0.008	0.017	-0.032	-0.002	0.008	- 0.067	-0.167	<b>-0.17</b>
SL	0.000	0.000	0.004	<b>0.000</b>	-0.002	-0.004	-0.005	0.017	-0.014	-0.001	-0.009	0.135	0.019	<b>0.14</b>
ML	0.001	0.002	0.008	0.000	<b>0.068</b>	0.018	0.102	-0.024	-0.086	-0.003	0.022	- 0.282	-0.334	<b>-0.51***</b>
EL	-0.002	-0.003	-0.010	0.000	-0.037	<b>-0.032</b>	-0.179	0.040	0.152	0.003	-0.034	0.417	0.534	<b>0.85***</b>
EG	-0.001	-0.002	-0.001	0.000	-0.025	-0.021	<b>-0.275</b>	0.099	0.191	0.000	-0.021	0.344	0.444	<b>0.73***</b>
HG	-0.001	-0.001	0.006	0.000	-0.012	-0.009	-0.190	<b>0.144</b>	0.043	-0.001	-0.009	0.190	0.199	<b>0.36***</b>
KL	-0.001	-0.002	-0.007	0.000	-0.026	-0.022	-0.231	0.027	<b>0.227</b>	0.001	-0.022	0.325	0.450	<b>0.72***</b>
RN	0.001	0.001	0.007	0.000	0.018	0.011	0.003	0.009	-0.014	<b>-0.010</b>	0.010	- 0.012	-0.225	<b>-0.2</b>
KR	-0.001	-0.002	-0.008	0.000	-0.031	-0.024	-0.124	0.029	0.105	0.002	<b>-0.047</b>	0.528	0.334	<b>0.76***</b>
SN	-0.002	-0.002	-0.005	0.000	-0.031	-0.022	-0.154	0.045	0.120	0.000	-0.040	<b>0.613</b>	0.328	<b>0.85***</b>
Wt	-0.002	-0.002	-0.012	0.000	-0.035	-0.027	-0.190	0.045	0.159	0.003	-0.024	0.313	<b>0.643</b>	<b>0.87***</b>

Here, DA= Days to anthesis, PH= Plant height (cm), EH= Ear height (cm), SL=Stalk lodging (%), ML= Moisture loss (%), EL= Ear length (cm), EG= Ear girth (cm), HG= Husk girth (cm), KL= Kernel length (cm), RN= Row numbers ear<sup>-1</sup>, KR= Kernel numbers row<sup>-1</sup>, SN= Seed numbers ear<sup>-1</sup>, Wt= 1000 seed weight (g), YP= Yield plant<sup>-1</sup> (g).

**Table 6.** Clustering of 15 maize genotypes

Cluster No.	No. of genotypes	Name of genotypes
I	3	G2, G1, G3
II	3	G10, G6, G8
III	2	G12, G14
IV	4	G4, G7, G11, G13
V	3	G5, G9, G15

**Table 7.** Cluster mean for different quantitative traits among 15 maize genotypes

Cluster No.	DA	PH	EH	SL	ML	EL	EG	HG	KL	RN	KR	SN	Wt	YP
I	107.50	144.86	94.33	17.96	24.56	11.85	12.31	9.01	3.30	15.89	20.81	290.39	151.67	46.35
II	94.44	178.75	82.61	17.41	13.78	20.15	15.82	9.92	5.90	14.39	31.00	441.64	370.83	163.08
III	98.50	145.46	67.88	12.72	14.54	16.97	12.96	8.73	4.23	13.58	25.08	325.50	287.25	91.80
IV	95.38	170.79	79.10	19.95	11.81	18.58	14.12	9.23	4.89	14.17	28.44	393.42	330.00	129.41
V	97.39	165.47	76.31	10.52	12.13	18.31	14.17	9.18	4.99	14.28	30.28	427.78	299.44	129.58

Here, DA= Days to anthesis (days), PH= Plant height (cm), EH= Ear height (cm), SL=Stalk lodging (%), ML= Moisture loss(%), EL= Ear length (cm), EG= Ear girth (cm), HG= Husk girth (cm), KL= Kernel Length (cm), RN= Row numbers ear<sup>-1</sup>, KR= Kernel numbers row<sup>-1</sup>, SN= Seed numbers ear<sup>-1</sup>, Wt= 1000 seed weight (g), YP= Yield plant<sup>-1</sup> (g).

**Table 8.** Percent Variance and cumulative (%) total variance of the Principal components (PCs) for morphological traits of 15 Maize genotypes under field condition

	Comp.1	Comp.2	Comp.3	Comp.4	Comp.5
DA	0.269	-0.235			-0.174
PH	-0.258	-0.316	0.293	0.401	-0.128
EH		-0.604	0.233	0.439	
SL		-0.211	-0.668	0.229	0.321
ML	0.242	-0.149		-0.195	
EL	-0.350				
EG	-0.316	-0.252	0.152	-0.352	
HG	-0.166	-0.385		-0.342	0.644
KL	-0.304		0.182	-0.224	-0.355
RN	0.109	-0.404	-0.263	-0.465	-0.456
KR	-0.300		-0.354	0.164	-0.154
SN	-0.314		-0.351		-0.22
Wt	-0.340	0.126	0.147		
YP	-0.371				
% Variance	47.3	11.9	8.9	8.4	6.2
Cumulative % total variance	47.3	59.2	68.1	76.5	82.7

Here, DA= Days to anthesis (days), PH= Plant height (cm), EH= Ear height (cm), SL=Stalk lodging (%), ML= Moisture loss (%), EL= Ear length (cm), EG= Ear girth (cm), HG= Husk girth (cm), KL= Kernel Length (cm), RN= Row numbers ear<sup>-1</sup>, KR= Kernel numbers row<sup>-1</sup>, SN= Seed numbers ear<sup>-1</sup>, Wt= 1000 seed weight (g), YP= Yield plant<sup>-1</sup> (g).

However plant height, ear length, ear girth, row numbers ear<sup>-1</sup> and kernel numbers row<sup>-1</sup> had direct negative effect on yield plant<sup>-1</sup>. But plant height, ear length, ear girth and kernel numbers row<sup>-1</sup> were positively correlated with yield plant<sup>-1</sup>. This positive effect of plant height mainly was due to the fact that negative direct effect of plant height on yield was nullified by its positive indirect effects via seed numbers ear<sup>-1</sup> and 1000 seed weight, so on for ear length and ear girth. Emer (2011) and Mohan *et al.* (2002) found the same result for plant height.

The residual effect determines how best the causal factors account for the variability of the dependent factor, the yield plant<sup>-1</sup> in this case. In case of the present study the residual effect was 0.115 indicating that the fourteen traits explain

88.5% of variability in yield plant<sup>-1</sup>. The reason seems to be very moderate and high significant correlation of some traits with yield.

The above information revealed that highly significant positive correlation with highest positive direct effect was observed in husk girth, kernel length, seed numbers ear<sup>-1</sup> and 1000 seed weight. So these traits could be considered as valued for yield improvement in these genotypes of maize.

### 3.4 Cluster analysis

Based on morphological diversity, fifteen maize genotypes were grouped into five clusters (Table 6). The distribution pattern revealed maximum number of genotypes in cluster IV is four in number (G4, G7, G11, G13), whilst other three

clusters (I, II, V) consists of three genotypes (G1, G2 and G3; G6, G8 and G10; G5, G9 and G15 respectively) and minimum number of genotypes (G12, G14) in cluster III. Subramanian and Subbaraman (2010) made dendrogram on 38 genotypes which results in four clusters. Similar results were reported by Singh *et al.* (2005) and Liu *et al.* (2006). Another study was carried out by Chen *et al.* (2007) reported that 186 maize genotypes were classified into ten clusters. Mean performance of different clusters for the traits studied reflected that all the short duration genotypes with higher yield were grouped into Cluster II whereas cluster I included long duration genotypes having lower yield indicating maximum contribution of these characters towards the divergence between Cluster I and II.

A wide range of variations for several characters among multi genotypic clusters were observed. However, the difference was clear for days to anthesis, plant height, stalk lodging (%), moisture loss (%), seed numbers ear<sup>-1</sup>, 1000 seed weight, and yield plant<sup>-1</sup> which has contributed largely to the total divergence. Hence, for the improvement of different characters viz., days to anthesis, plant height, ear length, ear girth, kernel length, Kernel numbers row<sup>-1</sup>, seed numbers ear<sup>-1</sup>, 1000 seed weight, yield plant<sup>-1</sup> under the present study, genotypes should be selected from cluster II, IV and V.

Thus hybridization among genotypes belonging to Cluster I and III with those of Cluster II, IV and V would exhibit higher heterosis for improvement of desirable traits in segregating populations. However, the objective of a plant breeder is not only to get high heterosis but also to achieve high level of production and reducing the life span of a variety so that, it can be fitted in existing cropping pattern.

### 3.5 Principal component analysis

The presence of broad phenotypic diversity among the maize genotypes was further substantiated by principal component analysis, which indicated that the total variation was fairly

distributed across all the morpho-agronomic traits. It was also quite conceivable that these traits were adequately represented by five principal components (accounting 82.07% of total variation) to measure underlying dimensions in the data. Principal components with their contribution to total variation were summarized here in table 8. The first PC which explained 47.3% of total variation was mainly associated with yield plant<sup>-1</sup>(g), ear length (cm), 1000 seed weight (g), ear girth (cm), seed numbers ear<sup>-1</sup> that are entirely different important yield related characters. Ear height (cm), plant height (cm), husk girth (cm), row numbers ear<sup>-1</sup> with a relatively highest negative weight were important in determining second principal axis (PC2) that accounted to the 11.9% variation. The third principal axis (PC3), accounting for 8.9% of the total variation, was governed by traits like stalk lodging (%), kernel numbers row<sup>-1</sup>, seed numbers ear<sup>-1</sup>. PC4 was associated with plant height, ear height, row numbers ear<sup>-1</sup>, ear girth (cm) and husk girth (cm). Traits like stalk lodging (%), husk girth, kernel length and row numbers ear<sup>-1</sup> contributed most to principal component 5. Our findings were in accordance to Hartings *et al.* (2008), indicating that traits related to the yield and size of plants contributed the most to the phenotypic variability between the accessions.

Beyene *et al.* (2006) measured 71.8% of the total variation in 62 traditional Ethiopian highland maize accessions was represented by the first four PCs. Azad *et al.* (2012) considered days to maturity, ear length, ear girth, yield per plant as important components of genetic divergence that also support our findings.

## 4. Conclusions

Significant variations were observed among the genotypes for all the traits, except stalk lodging (%) and row number ear<sup>-1</sup>. The estimated PCV is higher than GCV supporting environmental influences on phenotypic expression. Highest heritability (84.75) was observed in 1000 seed weight, followed by yield plant<sup>-1</sup> (82.61), ear

length (81.44), ear girth (80.2). High heritability with high genetic advance was observed for 1000 seed weight, seed numbers ear<sup>-1</sup> and yield plant<sup>-1</sup>. These traits can be improved through appropriate selection schemes. The research emphasized the need for selection based on plant with lower days to anthesis, higher seed numbers ear<sup>-1</sup>, high 1000-seed weight and plant height for yield improvement in maize genotypes as per the findings of the plant characters association. Assessing genetic diversity is basic for the utilization of germplasm. The research revealed adequate genetic diversity among studied 15 genotypes. BHM-7 performed best, other genotypes like E155-1, BHM-5 derived F<sub>2</sub> as non-hybrids were good enough considering yield and yield associated traits. All these good performing genotypes could be utilized to enhance frequencies of favorable alleles for quality, earliness and grain yield of maize.

#### References

- Ababulgu, D. A. 2014. Genetic diversity and combining ability of selected quality protein maize (QPM) inbred lines adapted to the highland agro-ecology of Ethiopia. University of Kwazulu-Natal, Republic of South Africa.
- Allard, R. 1975. Principles of plant breeding. John Wiley and Sons Inc., New York.
- Azad, M. A. K., Biswas, B. K., Alam, N. and Alam, S. K. S. 2012. Genetic diversity in maize (*Zea mays* L.) inbred lines. *The Agriculturists*, 10: 64-70.
- BBS 2016. Yearbook of Agricultural Statistics-2015, 27th series. Bangladesh Bureau of Statistics, Statistics and Informatics Division, Ministry of Planning, Government of People's Republic of Bangladesh (www.bbs.gov.bd).
- Beiragi, M. A., Ebrahimi, M., Mostafavi, K., Golbashy, M. and Khorasani, S. K. 2011. A study of morphological basis of corn (*Zea mays* L.) yield under drought stress condition using correlation and path coefficient analysis. *Journal of Cereals and Oilseeds*, 2:32-37.
- Bekele, A. and Rao, T.N. 2014. Estimates of heritability, genetic advance and correlation study for yield and its attributes in maize (*Zea mays* L.). *Journal of Plant Sciences*, 21: 4-6.
- Beyene, Y., Botha, M. A. and Myburg, A. A. 2005. A comparative study of molecular and morphological methods of describing genetic relationships in traditional Ethiopian highland maize. *African Journal of Biotechnology*, 4:586-595.
- Burton, G. W. 1952. Quantitative inheritance in grasses, *Proc. 6th Int. Grassland Cong* 1, 277-283.
- Chen, F.B., Yang, K.C., Rong, T.Z. and Pan, G. T. 2007. Analysis of genetic diversity of maize hybrids in the regional tests of Sichuan and Southwest China. *Acta Agronomica Sinica*, 33:991-998.
- Comstock, R., Robinson, H. and Gowen, J. 1952. Estimation of average dominance of genes, *Heterosis*, 494-516.
- Dewey, D.R. and Lu, K. H. 1959. A correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agronomy Journal*, 51:515-518.
- Emer, I. 2011. Correlation and path coefficient analysis in sweet corn. *Turkish Journal of Field Crops*, 16(2):105-107.
- Ghimire, B., Timsina, D. and Nepal, J. 2015. Analysis of chlorophyll content and its correlation with yield attributing traits on early varieties of maize (*Zea mays* L.). *Journal of Maize Research and Development*, 1(1):134-214.
- Hanson, W. D. 1961. Heritability, Statistical Genetics and Plant Breeding, National Academy of Science, National Research Council, Washington, 125-140.
- Hartings, H., Berardo, N., Mazzinelli, G. F., Valoti, P., Verderio, A. and Motto, M. 2008. Assessment of genetic diversity and

- relationships among maize (*Zea mays* L.) Italian landraces by morphological traits and AFLP profiling. *Theoretical and Applied Genetics*, 117:831-842.
- Johnson, H.W., Robinson, H. F. and Comstock, R. E. 1955. Estimation of genetic and environmental variability in soybean. *Journal of Agronomy*, 47:314-318.
- Kinfe, H. and Tsehaye, Y. 2015. Studies of heritability, genetic parameters, correlation and path coefficient in elite maize hybrids. *Academic Research Journal of Agricultural Science and Research*, 3(10):296-303.
- Liu, Y. A., Hou, J. H., Gao, J. Z. and Wei, Z. 2006. Principal component analysis and cluster analysis of introduced maize varieties. *Journal of Maize Science*, 14(2):16-18.
- Miller, P., Williams, J., Robinson, H. and Comstock, R. 1958. Estimates of genotypic and environmental variances and covariances in upland cotton and their implications in selection. *Agronomy Journal*, 50:126-131.
- Mohammadi, S. A., Prasanna, B. M. and Singh, N. N. 2003. Sequential path model for determining interrelationships among grain yield and related characters in maize. *Crop Science*, 43:1690-1697.
- Mohan, Y. C., Singh, D. K. and Rao, N. V. 2002. Path coefficient analysis for oil and grain yield in maize (*Zea mays* L.) genotypes. *National Journal of Plant Improvement*, 4:75-76.
- Munawar, M., Shahbaz, M., Hammad, G. and Yasir, M. 2013. Correlation and path analysis of grain yield components in exotic maize (*Zea mays* L.) hybrids. *International Journal of Sciences: Basic and Applied Research*, 12 (1): 2-27.
- Plummer, D. T. 1971. An Introduction to Practical Biochemistry, Tata McGraw-Hill Pub.Com. Ltd. Bombay, New Delhi.
- R Core Team. 2016. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria.
- Rafiq, C.M., Rafique, M., Hussain, V. and Altaf, V. 2010. Studies on heritability, correlation and path analysis in maize (*Zea mays* L.). *Agricultural Research*, 48(1):35-38.
- Rahman, S., Mia, M. M., Quddus, T., Hassan, L. and Haque, M. A. 2015. Assessing genetic diversity of maize (*Zea mays* L.) genotypes for agronomic traits. *Research in Agriculture, Livestock and Fisheries*, 2 (1): 53-61.
- Salami, A. E., Adegoke, S. A. O. and Adegbite, O. A. 2007. Genetic variability among maize cultivars grown in Ekiti-State, Nigeria. *Middle-East Journal of Science and Research*, 2(1):9-13.
- Singh, R. K. and Choudhury, B. D. 1985. Biometrical method in quantitative genetic analysis. Kalyani Publishers, Ludhiana, New Delhi, 54-57 pp.
- Singh, D. N., Sahu, A. and Parida, A. K. 1997. Genetic variability and correlation studies in tomato (*Lycopersicon esculentum* Mill.). *Journal of Environment and Ecology*, 15: 117-121.
- Singh, P., Sain, V., Dwivedi, V. K., Kumar, Y. and Sangwan, O. 2005. Genetic divergence studies in maize (*Zea mays* L.). *Annals of Agricultural and Biological Research*, 10(1):43-46.
- Subramanian, A. and Subbaraman, N. 2010. Hierarchical cluster analysis of genetic diversity in Maize germplasm. *Electronic Journal of Plant Breeding*, 1:431-436.
- Thompson, J. A., Nelson, R. L. and Vodkin, L. O. 1998. Identification of diverse soybean germplasm using RAPD markers. *Crop Science*, 38:1348-1355.
- Wright, S. 1921. Correlation and causation. *Journal of Agricultural Research*, 20:557-585.